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UniProtKB/Swiss-Prot entry Q80W54

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Entry information

Entry name	FACE1_MOUSE
Primary accession number	Q80W54
Secondary accession numbers	Q8BJK4 Q8K569
Integrated into Swiss-Prot on	September 13, 2005
Sequence was last modified on	September 13, 2005 (Sequence version 2)
Annotations were last modified on	September 2, 2008 (Entry version 35)
Name and origin of the protein	
Protein name	CAAX prenyl protease 1 homolog
Synonyms	EC 3.4.24.84 Prenyl protein-specific endoprotease 1 Farnesylated proteins-converting enzyme 1 FACE-1 Zinc metalloproteinase Ste24 homolog
Gene name	Name: Zmpste24 Synonyms: Face1
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii; Muroidea; Muridae; Murinæ; Mus.
Protein existence	1: Evidence at protein level;
References	

[1] NUCLEOTIDE SEQUENCE [mRNA].

DOI=10.1074/jbc.M102908200; PubMed=11399759 [NCBI, ExPASy, EBI, Israel, Japan]
 Leung G.K., Schmidt W.K., Bergo M.O., Gavino B., Wong D.H., Tam A., Ashby M.N., Michaelis S.,
 Young S.G.;
 "Biochemical studies of Zmpste24-deficient mice.";
J. Biol. Chem. 276:29051-29058(2001).

[2] NUCLEOTIDE SEQUENCE [mRNA], AND FUNCTION IN LAMIN A/C PROCESSING.

STRAIN=C57BL/6;

DOI=10.1038/ng871; PubMed=11923874 [NCBI, ExPASy, EBI, Israel, Japan]

Pendas A.M., Zhou Z., Cadinanos J., Freije J.M.P., Wang J., Hultenby K., Astudillo A., Wernerson A., Rodriguez F., Triggvason K., Lopez-Otin C.;

"Defective prelamin A processing and muscular and adipocyte alterations in Zmpste24 metalloproteinas deficient mice.;"

Nat. Genet. 31:94-99(2002).

[3] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].

STRAIN=C57BL/6J;

DOI=10.1126/science.1112014; PubMed=16141072 [NCBI, ExPASy, EBI, Israel, Japan]

Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Hayashizaki Y.;

"The transcriptional landscape of the mammalian genome.;"

Science 309:1559-1563(2005).

Comments

- **FUNCTION:** Proteolytically removes the C-terminal three residues of farnesylated proteins. Acts on lamin A/C.
- **CATALYTIC ACTIVITY:** The peptide bond hydrolyzed can be designated -C-| -A-A-X in which C is an S-isoprenylated cysteine residue, A is usually aliphatic and X is the C-terminal residue of the substrate protein, and may be any of several amino acids.
- **COFACTOR:** Binds 1 zinc ion per subunit (*By similarity*).
- **SUBCELLULAR LOCATION:** Endoplasmic reticulum membrane; Multi-pass membrane protein (*By similarity*). Golgi apparatus membrane; Multi-pass membrane protein (*By similarity*).
- **SIMILARITY:** Belongs to the peptidase M48A family [view classification].

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Cross-references

Sequence databases

AY029194; AAK38172.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

EMBL AJ487544; CAD31792.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]
AK083566; BAC38953.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

RefSeq NP_766288.1; -.

UniGene Mm.34399

3D structure databases

ModBase Q80W54.

Protein family/group databases

MEROps M48.003; -.

Organism-specific databases

MGI MGI:1890508; Zmpste24.

Gene expression databases

ArrayExpress Q80W54; -.

GermOnline ENSMUSG00000043207; Mus musculus.

Ontologies

GO:0005624; Cellular component: membrane fraction (*inferred from direct assay from MGI*)GO:0004222; Molecular function: metalloendopeptidase activity (*inferred from direct assay from MGI*).GO GO:0006998; Biological process: nuclear membrane organization (*inferred from genetic interaction from MGI*).

GO:0030327; Biological process: prenylated protein catabolic process (*inferred from direct assay from MG*).

QuickGo
view.

Family and domain databases

IPR006025; Pept_M_Zn_BS.
IPR001915; Peptidase_M48.
Graphical view of domain structure.
PF01435; Peptidase_M48; 1.
Pfam graphical view of domain structure.
PS00142; ZINC_PROTEASE; FALSE_NEG.
BLOCKS Q80W54.

Genome annotation databases

Ensembl ENSMUSG00000043207; Mus musculus. [Contig view]
GenoID 230709; -.
KEGG mmu:230709; -.

Phylogenomic databases

HOGENOM Q80W54; -.
HOVERGEN Q80W54; -.

Other

SOURCE Zmpste24; Mus musculus.
ProtoNet Q80W54.
UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Endoplasmic reticulum; Golgi apparatus; Hydrolase; Membrane; Metal-binding; Metalloprotease; Protease; Transmembrane; Zinc.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	475	475	CAAX prenyl protease 1 homolog.	PRO_0000138845
TRANSMEM	19	39	21	Potential.	
TRANSMEM	82	102	21	Potential.	
TRANSMEM	124	144	21	Potential.	
TRANSMEM	171	191	21	Potential.	
TRANSMEM	196	216	21	Potential.	
TRANSMEM	348	368	21	Potential.	
TRANSMEM	383	405	23	Potential.	
ACT_SITE	336	336		By similarity.	
ACT_SITE	419	419		Proton donor (By similarity).	
METAL	335	335		Zinc; catalytic (By similarity).	
METAL	339	339		Zinc; catalytic (By similarity).	
METAL	415	415		Zinc; catalytic (By similarity).	
CONFLICT	53	53		A -> S (in Ref. 2; CAD31792).	
CONFLICT	153	153		H -> Q (in Ref. 1; AAK38172).	
CONFLICT	157	157		H -> Q (in Ref. 1; AAK38172).	

Sequence information

Length: 475 AA [This is the length of the unprocessed precursor]

Molecular weight: 54735 Da [This is the MW of the unprocessed precursor]

CRC64: 509B82D757FC7A4B [This is a checksum on the sequence]

10	20	30	40	50	60
MGMWASVDAM	WDFPAEKRI	GAVLLFWSWT	YLWETFLAQR	QRRIYKTTTR	VPAELEQIMD
70	80	90	100	110	120
SDTIEKRSRLY	QLDKSTFSFW	SGLYSEVEGT	FILLFGGIPY	LWRLSGQFC	SAGFGPEYEI
130	140	150	160	170	180
IQSLVFLLLA	TLFSLATGLP	WSLYNTFVIE	EKHGFNHQTL	EFFMKDAIKK	FIVTQCILLP
190	200	210	220	230	240
VSALLYI	IGGDYFFIYA	WLFTLVVSLV	LVTIYADYIA	PLFDKFTPLP	EGKLKQEIEV
250	260	270	280	290	300
MAKSIDFPLT	KVYVVEGSKR	SSHSNAYFYG	FFKNKRIVLF	DTLLEEYSVP	NKDNQEESGM
310	320	330	340	350	360
EARNEGEGDS	EEVKAKVKNK	KQGCKNEEVL	AVLGHELGHW	KLGHTVKNII	ISQMNSFLCF
370	380	390	400	410	420
FLFAVLIGRR	ELFAAFGFYD	SQPTLIGLLI	IFQFIFSPYN	EVLSFCLTVL	SRRFEFQADA
430	440	450	460	470	
FAKKLGAKD	LYSALIKLNU	DNLGFPVSDW	LFSTWHYSHP	PLLERLQALK	NAKQD

Q80W54 in
FASTA format

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ExPASy/SIB
or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale,
Compute pI/Mw, PeptideMass, PeptideCutter,
Dotlet (Java)

 ScanProsite, MotifScan



Submit a homology modeling request to SWISS-MODEL

 NPSA Sequence analysis tools

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